REMARKS

Claims 27-38 remain pending in this application. No claims are amended in this paper.

An Advisory Action mailed July 26, 2005, requested that information submitted in the Appendix of Applicants' previously filed Response dated June 24, 2005 be submitted in the form of a declaration in order to be considered.

The sequence alignment set forth in the Appendix simply compared the sequences disclosed in the instant application with publicly available sequences using publicly available software. This alignment was submitted merely to facilitate the Examiner's evaluation of the sequences of the invention against publicly available sequences.

Section 716.02(g) of the MPEP states that the reason for requiring evidence to be in the form of an affidavit or declaration is to obtain assurances that any statements or representations are correct as provided by 35 USC §25 and 18 USC §1001. 35 USC §25 states that the "Director may by rule prescribe that any document to be filed in the Patent and Trademark Office **and** which is **required** by any law, rule or other regulation **to be under oath** may be subscribed to by a written declaration in such form as the Director may prescribe, such declaration to be in lieu of the oath otherwise required."

It is respectfully submitted that the submission of an alignment using publicly available software and information does not appear to be required by any law, rule or regulation to be under oath. Furthermore, one skilled in the art has access to the publicly available sequences and publicly available software. This situation is far-

removed from one in which experimental data set forth in laboratory notebook is being set forth in a declaration.

Specifically, the Appendix submitted with the aforementioned Response (also re-submitted herewith for the Examiner's convenience) is an alignment of the sequences disclosed in the instant application, specifically SEQ ID NO:8 and SEQ ID NO:6, with a publicly available sequence set forth in WO9748793. The information in the Appendix was generated by using publicly available software, namely the Megalign program of the LASERGENE v 6.1 bioinformatics computing suite (DNASTAR Inc., Madison, WI). More information regarding this software can be found at www.dnastar.com and from the enclosed printout from this website.

The multiple alignment in the Appendix was prepared using the Clustal method of alignment (Higgins and Sharp (1989) *CABIOS. 5*:151-153) with the default parameters (GAP PENALTY=10, GAP LENGTH PENALTY=10).

In view of the foregoing, it is respectfully submitted that the instant application is now in form for allowance which allowance is respectfully solicited.

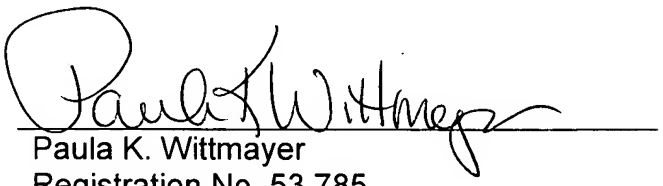
In the event that a telephone conference would facilitate examination of this application in any way, the Examiner is invited to contact the undersigned at the number provided.

AUTHORIZATION

The Commissioner is hereby authorized to charge any additional fees which may be required for the timely consideration of this amendment under 37 C.F.R. §§ 1.16 and 1.17, or credit any overpayment to Deposit Account No. 13-4500, Order No. 2119-4293.

Respectfully submitted,
MORGAN & FINNEGAN, L.L.P.

Dated: August 17, 2005

By: 
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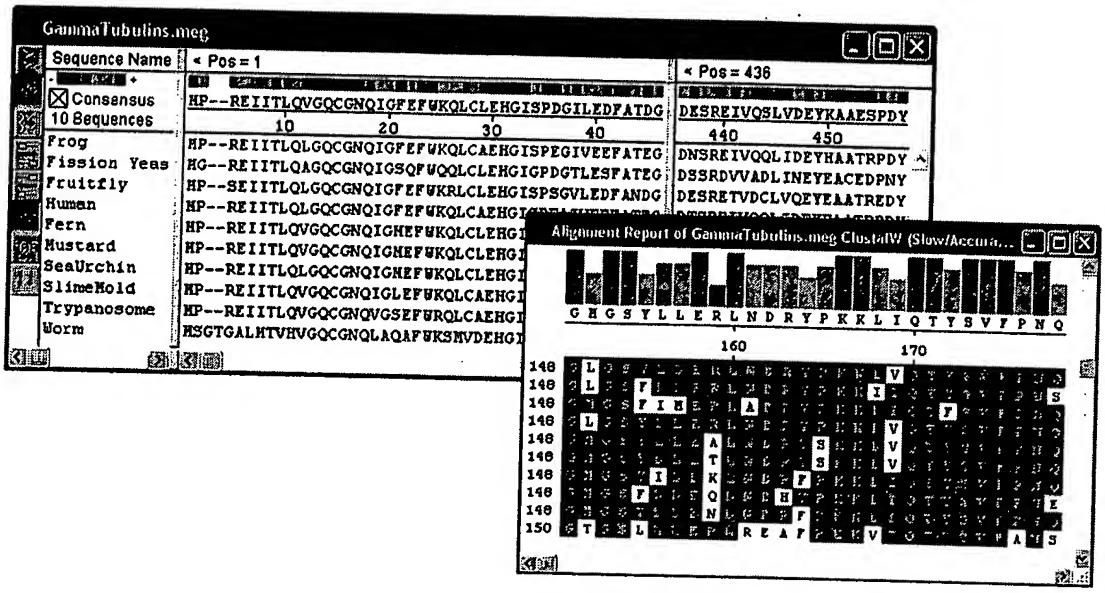
Appendix A

Appendix A shows a comparison of the amino acid sequences of sterol delta-14 reductase from soy clone SID ssm.pk0031.d12:fis (SEQ ID NO:8), src3c.pk009.c1:fis (SEQ ID NO: 6) and *Arabidopsis thaliana* (WO9748793). Amino acids conserved among all sequences are indicated with an asterisk (*) on the top row; dashes are used by the program to maximize alignment of the sequences. The method parameters used to produce the multiple alignment of the sequences below was performed using the Clustal method of alignment (Higgins and Sharp (1989) *CABIOS. 5*:151-153) with the default parameters (GAP PENALTY=10, GAP LENGTH PENALTY=10). SEQ ID NO's: 6 and 8 share 80.4 and 78% sequence identity, respectively, with the sequence claimed in WO 9748793.

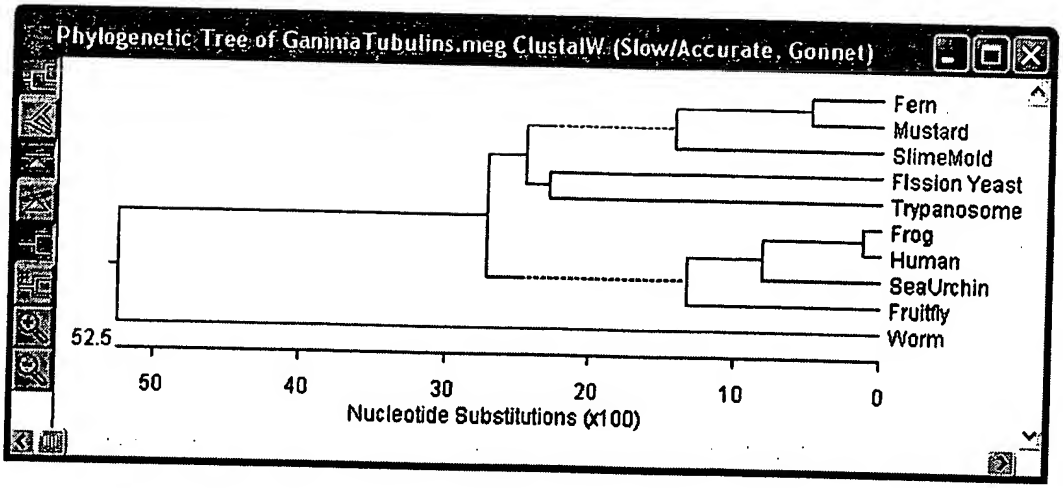
```
                *     *** **  *     **  **  * ****** *****   ** * **  * * **
SEQ ID NO:8 MMESHVDLGFLLQALTPSWNSVPLLVGFFTYLAVAGSILPGKLVPGVALLDGTRLHYCCN
SEQ ID NO:6 MMESHVDLGFLLQALTPSWNSVPLLVGFFTYLAVAGSILPGKLVPGVALLDGTRLHYCCN
WO9748793   MLL-DMDLGVLLPSL----QSVYVLVFYFVYLAVAGEILPGKVIRGVLLSDGSQLRYRCN

                *** * **** *** ** * ***    ******** ** *  **** *   *  *  ***
SEQ ID NO:8 GLLSLLLLVALLGIGAKMGFVSPTAISDRGLELLSTTFAFSFLVTLILHFSGCKSQSKGS
SEQ ID NO:6 GLLSLLLLVALLGIGAKMGFVSPTAISDRGLELLSTTFAFSFLVTLILHFSGCKSQSKGS
WO9748793   GLLALILLVAILGICAKLGIVSPLVVADRGLELLSATFIFCVLVTLALYVTGRSSSNKGS

                ***** **** ************** ** *     ************** ** *** ***
SEQ ID NO:8 SLKPHLSGNLIHDWWFGIQLNPQFMGIDLK-----AGMMGWLLINLSILMKSIQDGTLSQ
SEQ ID NO:6 SLKPHLSGNLIHDWWFGIQLNPQFMGIDLKFFFVRAGMMGWLLINLSILMKSIQDGTLSQ
WO9748793   SLKPHVSGNLVHDWWFGIQLNPQFMSIDLKFFFVRAGMMGWLLINLSILAKSVQDGSLSQ

                ****** ************************************ **** ********* *
SEQ ID NO:8 SMILYQLFCALYILDYFVHEEYMTSTWDIIAERLGFMLVFGDLVWIPFSFSIQGWWLLMN
SEQ ID NO:6 SMILYQLFCALYILDYFVHEEYMTSTWDIIAERLGFMLVFGDLVWIPFSFSIQGWWLLMN
WO9748793   SMILYQIFCALYILDYFVHEEYMTSTWDIIAERLGFMLVFGDLLWIPFTFSIQGWWLLHN

                 ****  *** ** ***************** ****** ******* * ***** *****
SEQ ID NO:8 SVELTPAAIVANCFVFLIGYMVFRGANKQKHVFKKNPKAPIWGKPPKVIGGKLLASGYWG
SEQ ID NO:6 SVELTPAAIVANCFVFLIGYMVFRGANKQKHVFKKNPKAPIWGKPPKVIGGKLLASGYWG
WO9748793   KVELTVPAIVVNCLVFLIGYMVFRGANKQKHIFKKNPKTPIWGKPPVVVGGKLLVSGYWG

                ********************* **** ***************** ** ************
SEQ ID NO:8 IARHCNYLGDLMLALSFSLPCGISSPIPYFYPIYLLILLIWRERTDEARCAEKYREIWAE
SEQ ID NO:6 IARHCNYLGDLMLALSFSLPCGISSPIPYFYPIYLLILLIWRERTDEARCAEKYREIWAE
WO9748793   IARHCNYLGDLMLALSFSLPCGISSPVPYFYPIYLLILLIWRERRDEVRCAEKYKEIWAE

                *  ***********
SEQ ID NO:8 YRKLVPWRILPYVY
SEQ ID NO:6 YRKLVPWRILPYVY
WO9748793   YLRLVPWRILPYVY
```

MegAlign™

Multiple and Pairwise Sequence Alignment



MegAlign offers you a choice of four pairwise and four multiple sequence alignment methods for aligning nucleic acid or polypeptide sequences. Enter your own sequences or load public data directly from NCBI*. If you want to find more related sequences for alignment, simply run a BLAST query or utilize the Entrez text query interface*, then drop in the sequences you want from the list of matches. Easily customize views of alignments to highlight the similarities or differences of the sequences. Differences in chemical, structural or functional characteristics between sequences can also be displayed as well as your own groupings or consensi. You may create a subalignment from the current alignment by simply selecting a sub-region. MegAlign also enables you to construct phylogenetic trees, generate detailed numerical reports or export data of sequence comparisons. Whether you want to compare gene families or sequence pairs, MegAlign provides you with flexible tools for customizing output for presentation and publication.



A module of:

Lasergene v6.0

DNA*
DNASTAR, Inc

DNASTAR, Inc. · tel: 608-258-7420 · e-mail: info@dnastar.com · www.dnastar.com

MegAlign™

MegAlign Features

Sequence Entry and Editing

- Import data from many popular file formats
- Read sequences and features from other Lasergene project files
- Edit template sequence and share newly created features through integration with SeqBuilder and other Lasergene modules
- Download sequences directly from NCBI* or a DNASTAR StarBlast database using accession numbers, BLAST or text searches

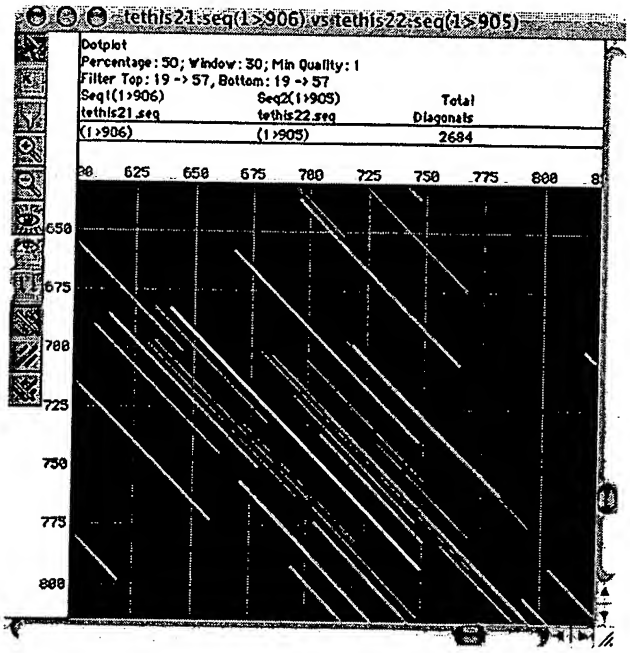
Graphical Displays and Tools

- Customize alignment displays by shading, boxing or hiding residues
- Highlight matches or mismatches to the consensus or other sequence with distinct colors or shading
- Define the consensus by residue or by chemical, structural, or charge characteristics
- Create a custom consensus based on your own residue classification scheme
- Display consensus strength as color-coded histograms
- Copy selected sections (rasters) of alignment report and paste into other applications

Alignments and Analyses

- Align DNA, protein and DNA+protein sequences
- Perform multiple sequence alignments using:
  - Jotun Hein
  - Clustal V
  - Clustal W - both Fast and Slow algorithms
- Perform pairwise sequence alignments using:
  - Wilbur-Lipman
  - Martinez Needleman-Wunsch
  - Lipman-Pearson
  - Dotplot analysis
- Create subalignments from selected ranges of longer alignments
- Reconstruct phylogeny
- Calculate sequence similarity and distance
- Edit and adjust final alignment manually if desired
- Export data and alignments into popular formats

*Requires Internet Connection



A module of:

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DNA*
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